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Display Show Send to Hide: ☐ sequence ☐ all but gene, CDS and mRNA

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☒ MGC

☐ 1: [BC016974](#). Reports Homo sapiens beta...[gi:16877455]

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LOCUS BC016974 1887 bp mRNA linear PRI 09-NOV-2001
 DEFINITION Homo sapiens, clone IMAGE:4393885, mRNA, partial cds.
 ACCESSION BC016974
 VERSION BC016974.1 GI:16877455
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM [Homo sapiens](#)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1887)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (05-NOV-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 27 Row: b Column: 11
 This clone was selected for full length sequencing because it
 passed the following selection criteria: GenomeScan gene
 prediction.

Differences found between this sequence and the human reference
 genome (build 36) are described in misc_difference features below.

FEATURES Location/Qualifiers
 source 1..1887
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"

CDS

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/clone="IMAGE:4393885"  
/tissue_type="Breast, mammary adenocarcinoma."  
/clone_lib="NIH_MGC_87"  
/lab_host="DH10B"  
/note="Vector: pCMV-SPORT6"  
<1..1151  
/codon_start=3  
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/protein_id="AAH16974.1"  
/db_xref="GI:16877456"  
/translation="RSGAGSCEEPSRRRRRARGRACSEWSLVSRSPVSALAGPLPLRR  
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LECNGAVSAHPNLHLPGSRDSPASASQVAGITDQLALFPQWKSTHYDVVGVLSARNN  
HELRNVIRSTWMRHLLQHPTLSQRVLVKFII GAHGCEVPVEDREDPYCKLLNITNPV  
LNQEIEAFSLSEDTSSGLPEDRVSVSVFRVLYPIVITSLGVFYDANDVGFQRNITVKL  
YQAEQEEALFIARFSPSPSCGVQVKNLWYKPVEQFILPESFEGTIVWESQDLHGLVSRN  
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misc_difference



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1875..1887  
/note="polyA tail: 13 bases do not align to the human  
genome."
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ORIGIN

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1  ggaggagcgg  ggccgggagc  tgcgaggagc  cctccagacg  tcgccgagcg  cgagggcggg  
61  cgtgctcgga  gtggtcgctc  gtcagccgcc  gccctcagc  ctccgcactt  gcaggtcccc  
121  tccctctccg  ccgggacgcg  ggagagcccg  gctcgcgcg  ggggcggcca  atgcgaaact  
181  ggctggtgct  gctgtgcccg  tgtgtgctcg  gggccgcgct  gcacctctgg  ctgcggctgc  
241  gctccccgcc  gcccgctgc  gcctccgggg  ccggccctgc  aggtggagtc  tcaactctgt  
301  tgcccaggct  ggagtgaat  ggcgcggtct  cggctcacc  caacctccac  ctcccgggtt  
361  caagagattc  tcctgcctca  gcctcccaag  tagctgggat  aacagatcag  ttggccttat  
421  ttcctcagtg  gaaatctact  cactatgatg  tggtagttgg  cgtgttgta  gctcgcaata  
481  accatgaact  tcgaaacgtg  ataagaagca  cctggatgag  acatttgcta  cagcatccca  
541  cattaagtca  acgtgtgctt  gtgaagttca  taataggtgc  tcatggctgt  gaagtgcctg  
601  tggaagacag  ggaagatcct  tattcctgta  aactactcaa  catcacaat  ccagttttga  
661  atcaggaaat  tgaagcgctt  agtctgtccg  aagacacttc  atcggggctg  cctgaggatc  
721  gagttgtcag  cgtgagtttc  cgagttctct  accccatcgt  tattaccagt  cttggagtg  
781  tctacgatgc  caatgatgtg  ggtttccaga  ggaacatcac  tgtcaaact  tatcaggcag  
841  aacaagagga  ggccctcttc  attgctcgct  tcagtcctcc  aagctgtggt  gtgcagggtg  
901  acaagctgtg  gtacaagccc  gtggaacaat  tcatcttacc  agagagcttt  gaaggtaaaa  
961  tcgtgtggga  gagccaagac  ctccacggcc  ttgtgtcaag  aaatctccac  aaagtgcag  
1021  tgaatgatgg  agggggagtt  ctcagagtc  ttacagctgg  ggaggggtg  ttgcctcatg  
1081  aattcttgga  aggtgtggag  ggagttgcag  gtggttttat  atatactatt  cagggttaag  
1141  ttgctagttg  aaacttgaaa  agtacactga  atgtcttaca  cttaatcttt  atacttgaga  
1201  gaaaaggatt  ttttcttttt  tgtcttttaa  aaaactttat  tcagataaaa  ttcacctttt  
1261  taaagtgggt  cagtggtttt  agtgtattct  tagagttcta  caaccggctc  cactcccaa  
1321  aaggaaaccc  cacaccatt  agcagttact  cctcattctt  acctcccaa  cccccacc  
1381  cctaacaact  actgatgcac  tttctttctc  tatggatttg  cctgttttga  acatttcaca  
1441  taaatggaaa  tgcacagtac  gtactctgtg  tgtcagtttc  tttgctgtaa  catgtgttcc  
1501  aggtctgtcc  attttgtatg  tatcagttat  tcttttttat  gatcatataa  tattctattg  
1561  catcgatatg  ccctatttta  ttcattcatt  aatggatgga  catttagatt  gcttctactt  
1621  tttgaatatg  aataattctg  tagtaaacad  gtaggtacaa  gtttttgtgt  ggtcatatat  
1681  ttccatttct  cttaaattgc  taggagtaga  agacctgggt  catataattg  tgtgtttaat  
1741  cacttgaggc  actgccaggt  tgttttttaa  agcagcagcc  cactttacat  ttccatagtc  
1801  agtatatgag  gattctagtt  tctccatatt  cttgtcaaca  cttaataaat  tgtctgtctt  
1861  ttaaaatata  ccaaaaaaaa  aaaaaaa
```

//

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Range: from to Features: ☒ CDD

☐ 1: [Q8NCR0](#). Reports UDP-GalNAc:beta-1...[gi:74751196]

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LOCUS Q8NCR0 500 aa linear PRI 04-DEC-2007
 DEFINITION UDP-GalNAc:beta-1,3-N-acetylgalactosaminyltransferase 2
 (Beta-1,3-N-acetylgalactosaminyltransferase II) (Beta-3-GalNAc-T2).
 ACCESSION Q8NCR0
 VERSION Q8NCR0.1 GI:74751196
 DBSOURCE swissprot: locus B3GL2_HUMAN, accession [Q8NCR0](#);
 class: standard.
 extra accessions:Q59GR3,Q5TCI3,Q96AL7
 created: Sep 5, 2006.
 sequence updated: Oct 1, 2002.
 annotation updated: Dec 4, 2007.
 xrefs: [AL135928.6](#), [CAI21727.1](#), [CAI21728.1](#), [BC016974.1](#), [AAH16974.1](#),
[BC029564.1](#), [AAH29564.1](#), [AB209046.1](#), [BAD92283.1](#)
 xrefs (non-sequence databases): RefSeq:[NP_689703.1](#),
 UniGene:[Hs.585040](#), Ensembl:[ENSG00000162885](#), GeneID:[148789](#),
 KEGG:[hsa:148789](#), HGNC:[28596](#), MIM:[610194](#), PharmGKB:[PA142672567](#),
 ArrayExpress:[Q8NCR0](#), CleanEx:[HS_B3GALNT2](#),
 GermOnline:[ENSG00000162885](#), InterPro:[IPR002659](#), PANTHER:[PTHR11214](#),
 Pfam:[PF01762](#)
 KEYWORDS Alternative splicing; Glycoprotein; Glycosyltransferase; Golgi
 apparatus; Membrane; Polymorphism; Signal-anchor; Transferase;
 Transmembrane.
 SOURCE Homo sapiens (human)
 ORGANISM [Homo sapiens](#)
[Eukaryota](#); [Metazoa](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Euteleostomi](#);
[Mammalia](#); [Eutheria](#); [Euarchontoglires](#); [Primates](#); [Haplorrhini](#);
[Catarrhini](#); [Hominidae](#); [Homo](#).
 REFERENCE 1 (residues 1 to 500)
 AUTHORS Gregory,S.G., Barlow,K.F., McLay,K.E., Kaul,R., Swarbreck,D.,
 Dunham,A., Scott,C.E., Howe,K.L., Woodfine,K., Spencer,C.C.,
 Jones,M.C., Gillson,C., Searle,S., Zhou,Y., Kokocinski,F.,
 McDonald,L., Evans,R., Phillips,K., Atkinson,A., Cooper,R.,
 Jones,C., Hall,R.E., Andrews,T.D., Lloyd,C., Ainscough,R.,
 Almeida,J.P., Ambrose,K.D., Anderson,F., Andrew,R.W., Ashwell,R.I.,
 Aubin,K., Babbage,A.K., Bagguley,C.L., Bailey,J., Beasley,H.,
 Bethel,G., Bird,C.P., Bray-Allen,S., Brown,J.Y., Brown,A.J.,
 Buckley,D., Burton,J., Bye,J., Carder,C., Chapman,J.C., Clark,S.Y.,
 Clarke,G., Clee,C., Cobley,V., Collier,R.E., Corby,N.,
 Coville,G.J., Davies,J., Deadman,R., Dunn,M., Earthrowl,M.,
 Ellington,A.G., Errington,H., Frankish,A., Frankland,J., French,L.,
 Garner,P., Garnett,J., Gay,L., Ghorri,M.R., Gibson,R., Gilby,L.M.,
 Gillett,W., Glithero,R.J., Grafham,D.V., Griffiths,C.,

Griffiths-Jones, S., Grocock, R., Hammond, S., Harrison, E.S., Hart, E., Haugen, E., Heath, P.D., Holmes, S., Holt, K., Howden, P.J., Hunt, A.R., Hunt, S.E., Hunter, G., Isherwood, J., James, R., Johnson, C., Johnson, D., Joy, A., Kay, M., Kershaw, J.K., Kibukawa, M., Kimberley, A.M., King, A., Knights, A.J., Lad, H., Laird, G., Lawlor, S., Leongamornlert, D.A., Lloyd, D.M., Loveland, J., Lovell, J., Lush, M.J., Lyne, R., Martin, S., Mashreghi-Mohammadi, M., Matthews, L., Matthews, N.S., McLaren, S., Milne, S., Mistry, S., Moore, M.J., Nickerson, T., O'Dell, C.N., Oliver, K., Palmeiri, A., Palmer, S.A., Parker, A., Patel, D., Pearce, A.V., Peck, A.I., Pelan, S., Phelps, K., Phillimore, B.J., Plumb, R., Rajan, J., Raymond, C., Rouse, G., Saenphimmachak, C., Sehra, H.K., Sheridan, E., Shownkeen, R., Sims, S., Skuce, C.D., Smith, M., Steward, C., Subramanian, S., Sycamore, N., Tracey, A., Tromans, A., Van Helmond, Z., Wall, M., Wallis, J.M., White, S., Whitehead, S.L., Wilkinson, J.E., Willey, D.L., Williams, H., Wilming, L., Wray, P.W., Wu, Z., Coulson, A., Vaudin, M., Sulston, J.E., Durbin, R., Hubbard, T., Wooster, R., Dunham, I., Carter, N.P., McVean, G., Ross, M.T., Harrow, J., Olson, M.V., Beck, S., Rogers, J., Bentley, D.R., Banerjee, R., Bryant, S.P., Burford, D.C., Burrill, W.D., Clegg, S.M., Dhami, P., Dovey, O., Faulkner, L.M., Gribble, S.M., Langford, C.F., Pandian, R.D., Porter, K.M. and Prigmore, E.

TITLE The DNA sequence and biological annotation of human chromosome 1

JOURNAL Nature 441 (7091), 315-321 (2006)

PUBMED [16710414](#)

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

Erratum:[Nature. 2006 Oct 26;443(7114):1013. Banerjee, R [added]; Bryant, SP [added]; Burford, DC [added]; Burrill, WDH [added]; Clegg, SM [added]; Dhami, P [added]; Dovey, O [added]; Faulkner, LM [added]; Gribble, SM [added]; Langford, CF [added]; Pandian, RD [added]; Porter, KM [added]; Prigmore, E [added]]

REFERENCE 2 (residues 1 to 500)

AUTHORS Gerhard, D.S., Wagner, L., Feingold, E.A., Shenmen, C.M., Grouse, L.H., Schuler, G., Klein, S.L., Old, S., Rasooly, R., Good, P., Guyer, M., Peck, A.M., Derge, J.G., Lipman, D., Collins, F.S., Jang, W., Sherry, S., Feolo, M., Misquitta, L., Lee, E., Rotmistrovsky, K., Greenhut, S.F., Schaefer, C.F., Buetow, K., Bonner, T.I., Haussler, D., Kent, J., Kiekhaus, M., Furey, T., Brent, M., Prange, C., Schreiber, K., Shapiro, N., Bhat, N.K., Hopkins, R.F., Hsie, F., Driscoll, T., Soares, M.B., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Piao, Y., Dudekula, D.B., Ko, M.S., Kawakami, K., Suzuki, Y., Sugano, S., Gruber, C.E., Smith, M.R., Simmons, B., Moore, T., Waterman, R., Johnson, S.L., Ruan, Y., Wei, C.L., Mathavan, S., Gunaratne, P.H., Wu, J., Garcia, A.M., Hulyk, S.W., Fuh, E., Yuan, Y., Sneed, A., Kowis, C., Hodgson, A., Muzny, D.M., McPherson, J., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madari, A., Young, A.C., Wetherby, K.D., Granite, S.J., Kwong, P.N., Brinkley, C.P., Pearson, R.L., Bouffard, G.G., Blakesly, R.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Griffith, M., Griffith, O.L., Krzywinski, M.I., Liao, N., Morin, R., Palmquist, D., Petrescu, A.S., Skalska, U., Smailus, D.E., Stott, J.M., Schnerch, A., Schein, J.E., Jones, S.J., Holt, R.A., Baross, A., Marra, M.A., Clifton, S., Makowski, K.A., Bosak, S. and Malek, J.

CONSRMT MGC Project Team

TITLE The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC)

JOURNAL Genome Res. 14 (10B), 2121-2127 (2004)

PUBMED [15489334](#)

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).

TISSUE=Mammary gland, and Testis
 Erratum:[Genome Res. 2006 Jun;16(6):804. Morrin, Ryan [corrected to Morin, Ryan]]

REFERENCE 3 (residues 1 to 500)
 AUTHORS Totoki,Y., Toyoda,A., Takeda,T., Sakaki,Y., Tanaka,A., Yokoyama,S., Ohara,O., Nagase,T. and Kikuno,R.F.
 TITLE Direct Submission
 JOURNAL Submitted (??-MAR-2005)
 REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 74-500 (ISOFORM 1).
 TISSUE=Brain

REFERENCE 4 (residues 1 to 500)
 AUTHORS Hiruma,T., Togayachi,A., Okamura,K., Sato,T., Kikuchi,N., Kwon,Y.D., Nakamura,A., Fujimura,K., Gotoh,M., Tachibana,K., Ishizuka,Y., Noce,T., Nakanishi,H. and Narimatsu,H.
 TITLE A novel human beta1,3-N-acetylgalactosaminyltransferase that synthesizes a unique carbohydrate structure, GalNAcbeta1-3GlcNAc
 JOURNAL J. Biol. Chem. 279 (14), 14087-14095 (2004)
 PUBMED [14724282](#)
 REMARK FUNCTION, BIOPHYSICOCHEMICAL PROPERTIES, GLYCOSYLATION, AND TISSUE SPECIFICITY.

REFERENCE 5 (residues 1 to 500)
 AUTHORS Sjoblom,T., Jones,S., Wood,L.D., Parsons,D.W., Lin,J., Barber,T.D., Mandelker,D., Leary,R.J., Ptak,J., Silliman,N., Szabo,S., Buckhaults,P., Farrell,C., Meeh,P., Markowitz,S.D., Willis,J., Dawson,D., Willson,J.K., Gazdar,A.F., Hartigan,J., Wu,L., Liu,C., Parmigiani,G., Park,B.H., Bachman,K.E., Papadopoulos,N., Vogelstein,B., Kinzler,K.W. and Velculescu,V.E.
 TITLE The consensus coding sequences of human breast and colorectal cancers
 JOURNAL Science 314 (5797), 268-274 (2006)
 PUBMED [16959974](#)
 REMARK VARIANT [LARGE SCALE ANALYSIS] SER-203.
 COMMENT On or before Sep 7, 2006 this sequence version replaced [gi:74707488](#), [gi:74746072](#), [gi:74731130](#).
 [FUNCTION] Beta-1,3-N-acetylgalactosaminyltransferase active in synthesizing a unique carbohydrate structure, GalNAc-beta-1-3GlcNAc, on N- and O-glycans. Has no galactose nor galactosaminyl transferase activity toward any acceptor substrate.
 [BIOPHYSICOCHEMICAL PROPERTIES] Kinetic parameters: KM=5.4 uM for UDP-GalNAc; KM=11 mM for GlcNAc-beta-Bn.
 [PATHWAY] Protein modification; protein glycosylation.
 [SUBCELLULAR LOCATION] Golgi apparatus membrane; Single-pass type II membrane protein (By similarity).
 [ALTERNATIVE PRODUCTS] Event=Alternative splicing; Named isoforms=2; Name=1; IsoId=Q8NCR0-1; Sequence=Displayed; Name=2; IsoId=Q8NCR0-2; Sequence=VSP_020250, VSP_020251, VSP_020252; Note=No experimental confirmation available.
 [TISSUE SPECIFICITY] Expressed in all tissues examined, but at highest levels in testis, adipose tissue, skeletal muscle and ovary.
 [PTM] N-glycosylated (Probable).
 [SIMILARITY] Belongs to the glycosyltransferase 31 family.
 [WEB RESOURCE] Name=GGDB; Note=GlycoGene database; URL=<http://ggdb.muse.aist.go.jp/GGDB/index.jsp>.

FEATURES
 source Location/Qualifiers
 1..500
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 gene 1..500
 /gene="B3GALNT2"

Protein 1..500
/gene="B3GALNT2"
/product="UDP-GalNAc:beta-1,
3-N-acetylgalactosaminyltransferase 2"
/EC_number="2.4.1.-"

Region 1..500
/gene="B3GALNT2"
/region_name="Mature chain"
/experiment="experimental evidence, no additional details
recorded"
/note="UDP-GalNAc:beta-1,3-N-
acetylgalactosaminyltransferase 2. /FTId=PRO_0000248362."

Region 1..6
/gene="B3GALNT2"
/region_name="Topological domain"
/inference="non-experimental evidence, no additional
details recorded"
/note="Cytoplasmic (Potential)."

Region 7..23
/gene="B3GALNT2"
/region_name="Transmembrane region"
/inference="non-experimental evidence, no additional
details recorded"
/note="Signal-anchor for type II membrane protein
(Potential)."

Region 24..500
/gene="B3GALNT2"
/region_name="Topological domain"
/inference="non-experimental evidence, no additional
details recorded"
/note="Lumenal (Potential)."

Region 37
/gene="B3GALNT2"
/region_name="Splicing variant"
/experiment="experimental evidence, no additional details
recorded"
/note="A -> AGGVSLLLPRLECNGAVSAHPNLHLPGRDSPASAS QVAGIT
(in isoform 2). /FTId=VSP_020250."

Site 116
/gene="B3GALNT2"
/site_type="glycosylation"
/inference="non-experimental evidence, no additional
details recorded"
/note="N-linked (GlcNAc...) (Potential)."

Site 174
/gene="B3GALNT2"
/site_type="glycosylation"
/inference="non-experimental evidence, no additional
details recorded"
/note="N-linked (GlcNAc...) (Potential)."

Region 203
/gene="B3GALNT2"
/region_name="Variant"
/experiment="experimental evidence, no additional details
recorded"
/note="N -> S (in a breast cancer sample; somatic
mutation). /FTId=VAR_035860."

Region 281..285
/gene="B3GALNT2"
/region_name="Splicing variant"

Region

/experiment="experimental evidence, no additional details recorded"
/note="EGDAL -> GK FAS (in isoform 2). /FTId=VSP_020251."
286..500

/gene="B3GALNT2"

/region_name="Splicing variant"

/experiment="experimental evidence, no additional details recorded"

Region

/note="Missing (in isoform 2). /FTId=VSP_020252."

307..457

/gene="B3GALNT2"

/region_name="Galactosyl_T"

/note="Galactosyltransferase. This family includes the galactosyltransferases

UDP-galactose:2-acetamido-2-deoxy-D-glucose3beta-galactosyltransferase and UDP-Gal:beta-GlcNAc beta 1,3-galactosyltransferase; pfam01762"

/db_xref="CDD:85659"

ORIGIN

```
1 mrnwlvlclp cvlgaalhlw lrlrspppac asgagpadql alfpqwksth ydvvvvgvlsa
61 rnnhelrnvi rstwmrhllq hptlsqrvlv kfiigahgce vpvedredpy sckllnitnp
121 vlnqeieafs lsedtssglp edrvsvsfr vlypivitsl gvfydandvg fqrnitvkly
181 qaeqeealfi arfsppscgv qvnklwykp v eqfilpesfe gtivwesqdl hglvsrnlhk
241 vtvdgggvl rvitagegal pheflegveg vaggfiytiq egdallhnlh srpqrldhi
301 rnlheedall keessiyddi vfvdvvdtyr nvpakllnfy rwtvettsfn lllktdddcy
361 idleavfnri vqknlbgpnf wwgfnrlnwa vdrtgkwqel eyppaypaf acgsgyvisk
421 divkwlasns grlkyqged vsmgiwmaai gpkryqdslw lcektcetgm lsspqyspwe
481 ltelwklker cgdpcrcqar
```

//

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Display Show Hide: ☐ sequence ☐ all but gene, CDS and mRNA

Range: from to ☐ Reverse complemented strand Features:

☐ 1: [AK035259](#). Reports *Mus musculus* adul...[gi:26330547]

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[Comment](#) [Features](#) [Sequence](#)

LOCUS AK035259 2399 bp mRNA linear HTC 05-DEC-2002
 DEFINITION *Mus musculus* adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530006I10 product:hypothetical Glycosyltransferase family 31 containing protein, full insert sequence.
 ACCESSION AK035259
 VERSION AK035259.1 GI:26330547
 KEYWORDS HTC; CAP trapper.
 SOURCE *Mus musculus* (house mouse)
 ORGANISM *Mus musculus*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 PUBMED [10349636](#)

REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 PUBMED [11042159](#)

REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 PUBMED [11076861](#)

REFERENCE 4
 AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,

Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.

TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 PUBMED [11217851](#)
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 2399)
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:<http://genome.gsc.riken.go.jp/>, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL:<http://genome.gsc.riken.go.jp/>
 URL:<http://fantom.gsc.riken.go.jp/>.

FEATURES
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ORIGIN




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//

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Aug 28 2007 16:53:42

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☐ **1: Q8BG28.** Reports UDP-GalNAc:beta-1...[gi:81895977]

[BLink](#), [Conserved Domains](#), [Links](#)

[Comment](#) [Features](#) [Sequence](#)

LOCUS Q8BG28 504 aa linear ROD 23-OCT-2007

DEFINITION UDP-GalNAc:beta-1,3-N-acetylgalactosaminyltransferase 2
(Beta-1,3-N-acetylgalactosaminyltransferase II) (Beta-3-GalNAc-T2)
(mbeta-3-GalNAc-T2).

ACCESSION Q8BG28

VERSION Q8BG28.1 GI:81895977

DBSOURCE swissprot: locus B3GL2_MOUSE, accession [Q8BG28](#);
class: standard.
extra accessions: Q5U4F9, Q8BXL0
created: Sep 5, 2006.
sequence updated: Mar 1, 2003.
annotation updated: Oct 23, 2007.
xrefs: [AB116655.1](#), [BAD13421.1](#), [AK035259.1](#), [BAC29004.1](#), [AK041022.1](#),
[BAC30784.1](#), [AK044785.1](#), [BAC32091.1](#), [AK084275.1](#), [BAC39153.1](#),
[AK151677.1](#), [BAE30602.1](#), [AK153362.1](#), [BAE31934.1](#), [AK167635.1](#),
[BAE39686.1](#), [BC085110.1](#), [AAH85110.1](#)
xrefs (non-sequence databases): RefSeq: [NP_848755.1](#),
UniGene: [Mm.21686](#), Ensembl: [ENSMUSG00000039242](#), GeneID: [97884](#),
KEGG: [mmu:97884](#), MGI: [2145517](#), ArrayExpress: [Q8BG28](#),
GermOnline: [ENSMUSG00000039242](#), InterPro: [IPR002659](#),
PANTHER: [PTHR11214](#), Pfam: [PF01762](#)

KEYWORDS Alternative splicing; Glycoprotein; Glycosyltransferase; Golgi
apparatus; Membrane; Signal-anchor; Transferase; Transmembrane.

SOURCE Mus musculus (house mouse)

ORGANISM [Mus musculus](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (residues 1 to 504)

AUTHORS Hiruma, T., Togayachi, A., Okamura, K., Sato, T., Kikuchi, N.,
Kwon, Y. D., Nakamura, A., Fujimura, K., Gotoh, M., Tachibana, K.,
Ishizuka, Y., Noce, T., Nakanishi, H. and Narimatsu, H.

TITLE A novel human beta1,3-N-acetylgalactosaminyltransferase that
synthesizes a unique carbohydrate structure, GalNAcbeta1-3GlcNAc

JOURNAL J. Biol. Chem. 279 (14), 14087-14095 (2004)

PUBMED [14724282](#)

REMARK NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND TISSUE SPECIFICITY.

REFERENCE 2 (residues 1 to 504)

AUTHORS Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M. C.,
Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R.,
Shimokawa, K., Bajic, V. B., Brenner, S. E., Batalov, S., Forrest, A. R.,
Zavolan, M., Davis, M. J., Wilming, L. G., Aidinis, V., Allen, J. E.,

Ambesi-Impiombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L., Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Huminiecki, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasaki, Y., Kelso, J., Kitamura, H., Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavesi, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugiura, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessy, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watahiki, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.

CONSRTM

FANTOM Consortium; RIKEN Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group)

TITLE

The transcriptional landscape of the mammalian genome

JOURNAL

Science 309 (5740), 1559-1563 (2005)

PUBMED

16141072

REMARK

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).

STRAIN=C57BL/6J; TISSUE=Aorta, Bone marrow, Eye, Placenta, Retina, Urinary bladder, and Vein

Erratum:[Science. 2006 Mar 24;311(5768):1713]

REFERENCE

3 (residues 1 to 504)

AUTHORS

Gerhard, D.S., Wagner, L., Feingold, E.A., Shenmen, C.M., Grouse, L.H., Schuler, G., Klein, S.L., Old, S., Rasooly, R., Good, P., Guyer, M., Peck, A.M., Derge, J.G., Lipman, D., Collins, F.S., Jang, W., Sherry, S., Feolo, M., Misquitta, L., Lee, E., Rotmistrovsky, K., Greenhut, S.F., Schaefer, C.F., Buetow, K., Bonner, T.I., Haussler, D., Kent, J., Kiekhaus, M., Furey, T., Brent, M., Prange, C., Schreiber, K., Shapiro, N., Bhat, N.K., Hopkins, R.F., Hsie, F., Driscoll, T., Soares, M.B., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Piao, Y., Dudekula, D.B., Ko, M.S., Kawakami, K., Suzuki, Y., Sugano, S., Gruber, C.E., Smith, M.R., Simmons, B., Moore, T., Waterman, R., Johnson, S.L., Ruan, Y., Wei, C.L., Mathavan, S., Gunaratne, P.H., Wu, J., Garcia, A.M., Hulyk, S.W., Fuh, E., Yuan, Y., Sneed, A., Kowis, C., Hodgson, A., Muzny, D.M., McPherson, J., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madari, A., Young, A.C., Wetherby, K.D., Granite, S.J., Kwong, P.N., Brinkley, C.P., Pearson, R.L., Bouffard, G.G., Blakesly, R.W.,

Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Griffith, M., Griffith, O.L., Krzywinski, M.I., Liao, N., Morin, R., Palmquist, D., Petrescu, A.S., Skalska, U., Smailus, D.E., Stott, J.M., Schnerch, A., Schein, J.E., Jones, S.J., Holt, R.A., Baross, A., Marra, M.A., Clifton, S., Makowski, K.A., Bosak, S. and Malek, J.

CONSRTM MGC Project Team

TITLE The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC)

JOURNAL Genome Res. 14 (10B), 2121-2127 (2004)

PUBMED [15489334](#)

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
TISSUE=Trophoblast stem cell
Erratum:[Genome Res. 2006 Jun;16(6):804. Morrin, Ryan [corrected to Morin, Ryan]]

COMMENT On or before Sep 7, 2006 this sequence version replaced [gi:81883617](#), [gi:81897952](#).
[FUNCTION] Beta-1,3-N-acetylgalactosaminyltransferase active in synthesizing a unique carbohydrate structure, GalNAc-beta-1-3GlcNAc, on N- and O-glycans. Has no galactose nor galactosaminyl transferase activity toward any acceptor substrate (By similarity).
[PATHWAY] Protein modification; protein glycosylation.
[SUBCELLULAR LOCATION] Golgi apparatus membrane; Single-pass type II membrane protein (By similarity).
[ALTERNATIVE PRODUCTS] Event=Alternative splicing; Named isoforms=2; Name=1; IsoId=Q8BG28-1; Sequence=Displayed; Name=2; IsoId=Q8BG28-2; Sequence=VSP_020253, VSP_020254; Note=No experimental confirmation available.
[TISSUE SPECIFICITY] Present in testis (at protein level). In testis, it is mainly detected in the middle layers of seminiferous tubules at stages XII to II. Strongly expressed in primary and secondary spermatocytes and early round spermatids, but not in spermatogonia, elongating or elongated spermatids, or in Leydig or Sertoli cells.
[PTM] N-glycosylated (By similarity).
[SIMILARITY] Belongs to the glycosyltransferase 31 family.

FEATURES

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Region /note="Cytoplasmic (Potential)."
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Region 60
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Site 176
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/note="N-linked (GlcNAc...) (Potential)."

Region 188..209
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/db_xref="CDD:85659"

Region 406
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/note="S -> G (in Ref. 3; AAH85110)."

ORIGIN

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NCBI Nucleotide

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Display Show Send to Hide: ☐ sequence ☐ all but gene, CDS and mRNA

Range: from to ☐ Reverse complemented strand Features:

☐ 1: [AK035259](#). Reports *Mus musculus* adul...[gi:26330547]

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LOCUS AK035259 2399 bp mRNA linear HTC 03-OCT-2006

DEFINITION *Mus musculus* adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530006I10 product:hypothetical Glycosyltransferase family 31 containing protein, full insert sequence.

ACCESSION AK035259

VERSION AK035259.1 GI:26330547

KEYWORDS HTC; HTC_FLI; CAP trapper.

SOURCE *Mus musculus* (house mouse)

ORGANISM *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

PUBMED [10349636](#)

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

PUBMED [11042159](#)

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

PUBMED [11076861](#)

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,

Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

PUBMED [11217851](#)

REFERENCE 5

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasaki,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

CONSRTM FANTOM Consortium; RIKEN Genome Exploration Research Group Phase I & II Team

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

PUBMED [12466851](#)

REFERENCE 6

AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M.,

Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Huminiecki, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasaki, Y., Kelso, J., Kitamura, H., Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavesi, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugiura, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessy, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watahiki, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.

CONSRTM

FANTOM Consortium; RIKEN Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group)

TITLE

The transcriptional landscape of the mammalian genome

JOURNAL

Science 309 (5740), 1559-1563 (2005)

PUBMED

[16141072](#)

REMARK

Erratum:[Science. 2006 Mar 24;311(5768):1713]

REFERENCE

7

AUTHORS

Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.

CONSRTM

RIKEN Genome Exploration Research Group; Genome Science Group (Genome Network Project Core Group); FANTOM Consortium

TITLE

Antisense transcription in the mammalian transcriptome

JOURNAL

Science 309 (5740), 1564-1566 (2005)

PUBMED

[16141073](#)

REFERENCE

8 (bases 1 to 2399)

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers
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